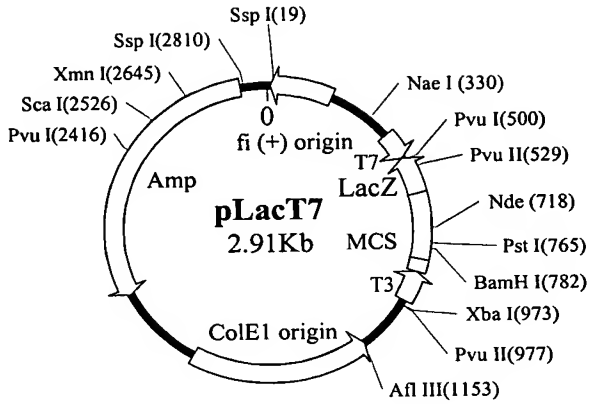
Figure 1

```
5'               11           21           31           41           51
+1   M  C  D  L  P  Q  T  H  S  L  G  N  R  R  A  L  I  L  L  A
1    ATGTGCGACC   TGCCGCAGAC   CCACTCCCTG   GGTAACCGTC   GTGCTCTGAT   CCTGCTGGCT
     TACACGCTGG   ACGGCGTCTG   GGTGAGGGAC   CCATTGGCAG   CACGAGACTA   GGACGACCGA

5'               71           81           91           101          111
+1   Q  M  R  R  I  S  P  F  S  C  L  K  D  R  H  D  F  G  F  P
61   CAGATGCGTC   GTATCTCCCC   GTTCTCCTGC   CTGAAAGACC   GTCACGACTT   CGGTTTCCCG
     GTCTACGCAG   CATAGAGGGG   CAAGAGGACG   GACTTTCTGG   CAGTGCTGAA   GCCAAAGGGC

5'               131          141          151          161          171
+1   Q  E  E  F  D  G  N  Q  F  Q  K  A  Q  A  I  S  V  L  H  E
121  CAGGAAGAAT   TCGACGGTAA   CCAGTTCCAG   AAAGCTCAGG   CTATCTCCGT   TCTGCACGAA
     GTCCTTCTTA   AGCTGCCATT   GGTCAAGGTC   TTTCGAGTCC   GATAGAGGCA   AGACGTGCTT

5'               191          201          211          221          231
+1   M  I  Q  Q  T  F  N  L  F  S  T  K  D  S  S  A  A  W  D  E
181  ATGATCCAGC   AGACCTTCAA   CCTGTTCTCC   ACCAAAGACT   CCTCCGCTGC   TTGGGACGAA
     TACTAGGTCG   TCTGGAAGTT   GGACAAGAGG   TGGTTTCTGA   GGAGGCGACG   AACCCTGCTT

5'               251          261          271          281          291
+1   S  L  L  E  K  F  Y  T  E  L  Y  Q  Q  L  N  D  L  E  A  C
241  TCCCTGCTGG   AAAAATTCTA   CACCGAACTG   TACCAGCAGC   TGAACGACCT   GGAAGCTTGC
     AGGGACGACC   TTTTTAAGAT   GTGGCTTGAC   ATGGTCGTCG   ACTTGCTGGA   CCTTCGAACG

5'               311          321          331          341          351
+1   V  I  Q  E  V  G  V  E  E  T  P  L  M  N  V  D  S  I  L  A
301  GTTATCCAGG   AAGTTGGTGT   TGAAGAAACC   CCGCTGATGA   ACGTTGACTC   CATCCTGGCT
     CAATAGGTCC   TTCAACCACA   ACTTCTTTGG   GGCGACTACT   TGCAACTGAG   GTAGGACCGA

5'               371          381          391          401          411
+1   V  K  K  Y  F  Q  R  I  T  L  Y  L  T  E  K  K  Y  S  P  C
361  GTTAAAAAAT   ACTTCCAGCG   TATCACCCTG   TACCTGACCG   AAAAAAAATA   CTCCCCGTGC
     CAATTTTTTA   TGAAGGTCGC   ATAGTGGGAC   ATGGACTGGC   TTTTTTTTAT   GAGGGGCACG

5'               431          441          451          461          471
+1   A  W  E  V  V  R  A  E  I  M  R  S  F  S  L  S  T  N  L  Q
421  GCTTGGGAAG   TTGTTCGTGC   TGAAATCATG   CGTTCCTTCT   CCCTGTCCAC   CAACCTGCAG
     CGAACCCTTC   AACAAGCACG   ACTTTAGTAC   GCAAGGAAGA   GGGACAGGTG   GTTGGACGTC

5'               491          501
+1   E  R  L  R  R  K  E  #
481  GAACGTCTGC   GTCGTAAAGA   ATAA
     CTTGCAGACG   CAGCATTTCT   TATT
```

Figure 2

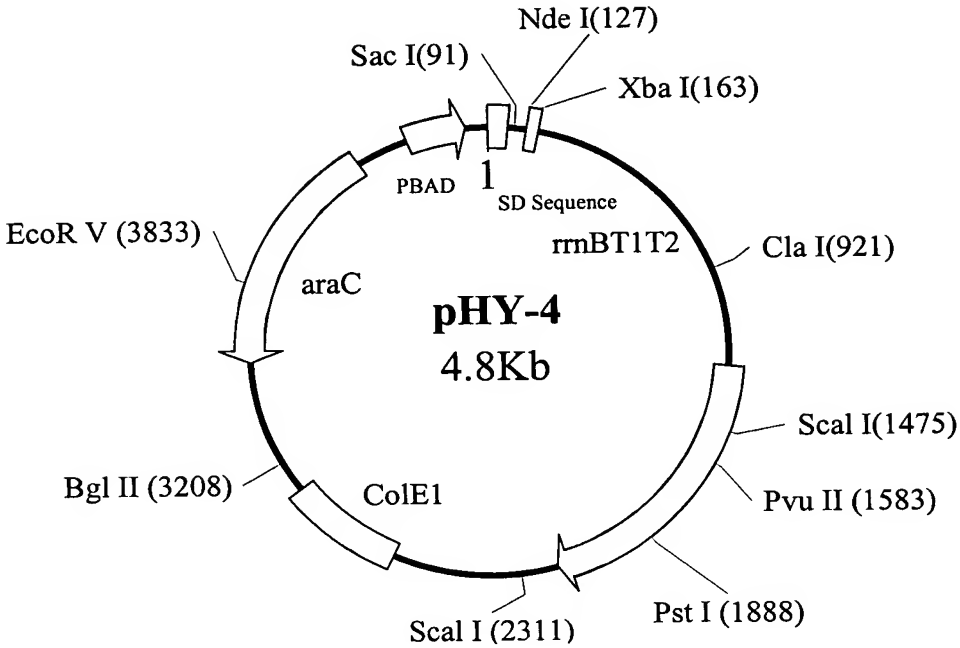
```
5'              11             21             31             41             51
+1  M  C  D   L  P  Q  T   H  S  L   G  N  R   R  A  L  I   L  L  A
  1 ATGTGTGATT TACCTCAAAC TCATTCTCTT GGTAACCGTC GCGCTCTGAT TCTGCTGGCA
    TACACACTAA ATGGAGTTTG AGTAAGAGAA CCATTGGCAG CGCGAGACTA AGACGACCGT

5'              71             81             91             1              11
+1  Q  M  R   R  I  S  P   F  S  C   L  K  D   R  H  D  F   G  F  P
 61 CAGATGCGTC GTATTTCCCC GTTTAGCTGC CTGAAAGACC GTCACGACTT CGGCTTTCCG
    GTCTACGCAG CATAAAGGGG CAAATCGACG GACTTTCTGG CAGTGCTGAA GCCGAAAGGC

5'              31             41             51             61             71
+1  Q  E  E   F  D  G  N   Q  F  Q   K  A  Q   A  I  S  V   L  H  E
121 CAAGAAGAGT TCGATGGCAA CCAATTCCAG AAAGCTCAGG CAATCTCTGT ACTGCACGAA
    GTTCTTCTCA AGCTACCGTT GGTTAAGGTC TTTCGAGTCC GTTAGAGACA TGACGTGCTT

5'              91             1              11             21             31
+1  M  I  Q   Q  T  F  N   L  F  S   T  K  D   S  S  A  A   W  D  E
181 ATGATCCAAC AGACCTTCAA CCTGTTTTCC ACTAAAGACA GCTCTGCTGC TTGGGACGAA
    TACTAGGTTG TCTGGAAGTT GGACAAAAGG TGATTTCTGT CGAGACGACG AACCCTGCTT

5'              51             61             71             81             91
+1  S  L  L   E  K  F  Y   T  E  L   Y  Q  Q   L  N  D  L   E  A  C
241 AGCTTGCTGG AGAAGTTCTA CACTGAACTG TATCAGCAGC TGAACGACCT GGAAGCATGC
    TCGAACGACC TCTTCAAGAT GTGACTTGAC ATAGTCGTCG ACTTGCTGGA CCTTCGTACG

5'              11             21             31             41             51
+1  V  I  Q   E  V  G  V   E  E  T   P  L  M   N  V  D  S   I  L  A
301 GTAATCCAGG AAGTTGGTGT AGAAGAGACT CCGCTGATGA ACGTCGACTC TATTCTGGCA
    CATTAGGTCC TTCAACCACA TCTTCTCTGA GGCGACTACT TGCAGCTGAG ATAAGACCGT
```

Figure 3



Ssp I(19)
Ssp I(2810)
Xmn I(2645)
Sca I(2526)
Pvu I(2416)
Nae I (330)
Pvu I(500)
Pvu II(529)
Nde (718)
Pst I(765)
BamH I(782)
Xba I(973)
Pvu II(977)
Afl III(1153)
0
fi (+) origin
T7
LacZ
Amp
pLacT7
2.91Kb
MCS
T3
ColE1 origin

Figure 4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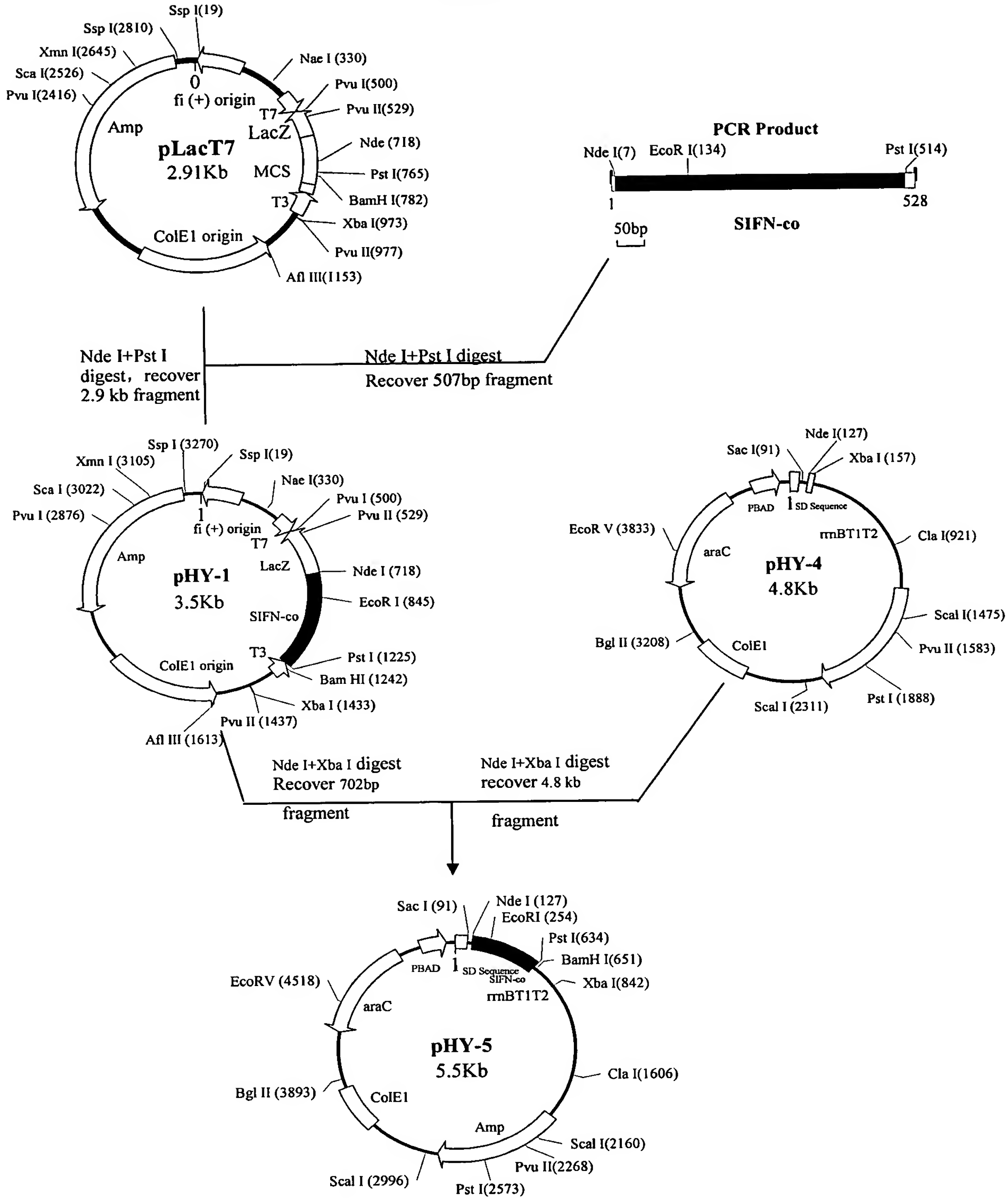
Sac I(91)
Xba I(163)
PBAD
1
SD Sequence
EcoR V (3833)
rrnBT1T2
Cla I(921)
araC
pHY-4
4.8Kb
ScaI I(1475)
Pvu II (1583)
Bgl II (3208)
ColE1
Pst I (1888)
ScaI I (2311)

Figure 5



Ssp I(19)
Ssp I(2810)
Xmn I(2645)
Sca I(2526)
Pvu I(2416)
Nae I (330)
Pvu I(500)
Pvu II(529)
Nde (718)
Pst I(765)
BamH I(782)
Xba I(973)
Pvu II(977)
Afl III(1153)
0
fi (+) origin
T7
Amp
LacZ
pLacT7
2.91Kb
MCS
T3
ColE1 origin
PCR Product
Nde I(7)
EcoR I(134)
Pst I(514)
1
528
50bp
SIFN-co
Nde I+Pst I
digest, recover
2.9 kb fragment
Nde I+Pst I digest
Recover 507bp fragment
Ssp I (3270)
Ssp I(19)
Xmn I (3105)
Sca I (3022)
Pvu I (2876)
Nae I(330)
Pvu I (500)
Pvu II (529)
Nde I (718)
EcoR I (845)
Pst I (1225)
Bam HI (1242)
Xba I (1433)
Pvu II (1437)
Afl III (1613)
1
fi (+) origin
T7
Amp
LacZ
pHY-1
3.5Kb
SIFN-co
T3
ColE1 origin
Nde I(127)
Sac I(91)
Xba I (157)
PBAD
1 SD Sequence
EcoR V (3833)
rrnBT1T2
Cla I(921)
araC
pHY-4
4.8Kb
ScaI (1475)
Bgl II (3208)
ColE1
Pvu II (1583)
Pst I (1888)
ScaI (2311)
Nde I+Xba I digest
Recover 702bp
fragment
Nde I+Xba I digest
recover 4.8 kb
fragment
Sac I (91)
Nde I (127)
EcoRI (254)
Pst I(634)
BamH I(651)
Xba I(842)
EcoRV (4518)
PBAD
1 SD Sequence
SIFN-co
rrnBT1T2
araC
pHY-5
5.5Kb
Cla I(1606)
Bgl II (3893)
ColE1
Amp
ScaI(2160)
Pvu II(2268)
ScaI (2996)
Pst I(2573)

Figure 6-A

Circular Dichroism spectra

Tested by Analysis and Measurment Center of Sichuan University.

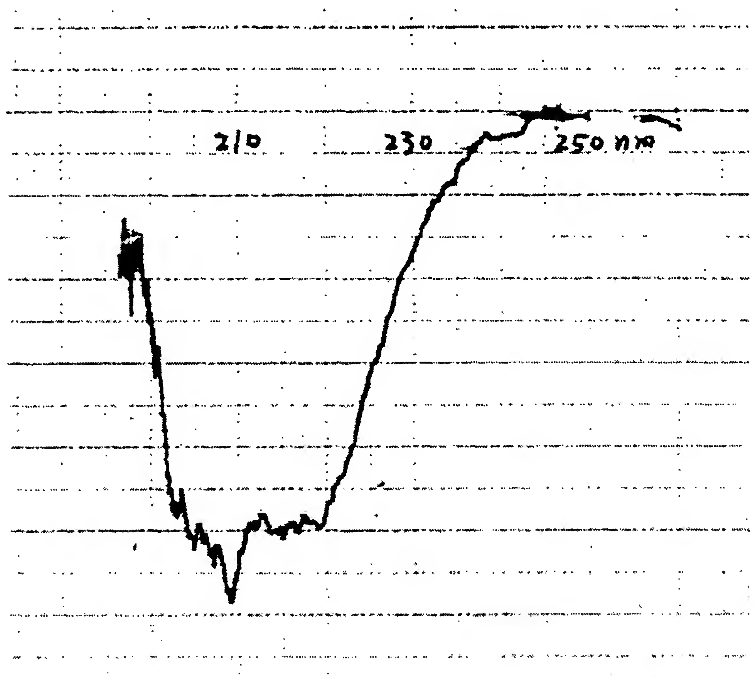


Fig 6-A Circular Dichroism spectrum of Infergen

Spectrum range: 250nm - 190nm

Sensitivity: 2 m°/cm

Light path: 0.20 cm

Equipment: Circular Dichroism J-500C

Samples :contain 30μg/ml IFN-con1, 5.9 mg/ml of NaCl and 3.8 mg/ml of Na_2PO_4, pH7.0.

Figure 6-B

HUMAN ALPHA SPECIES CONSENSUS IFN 495

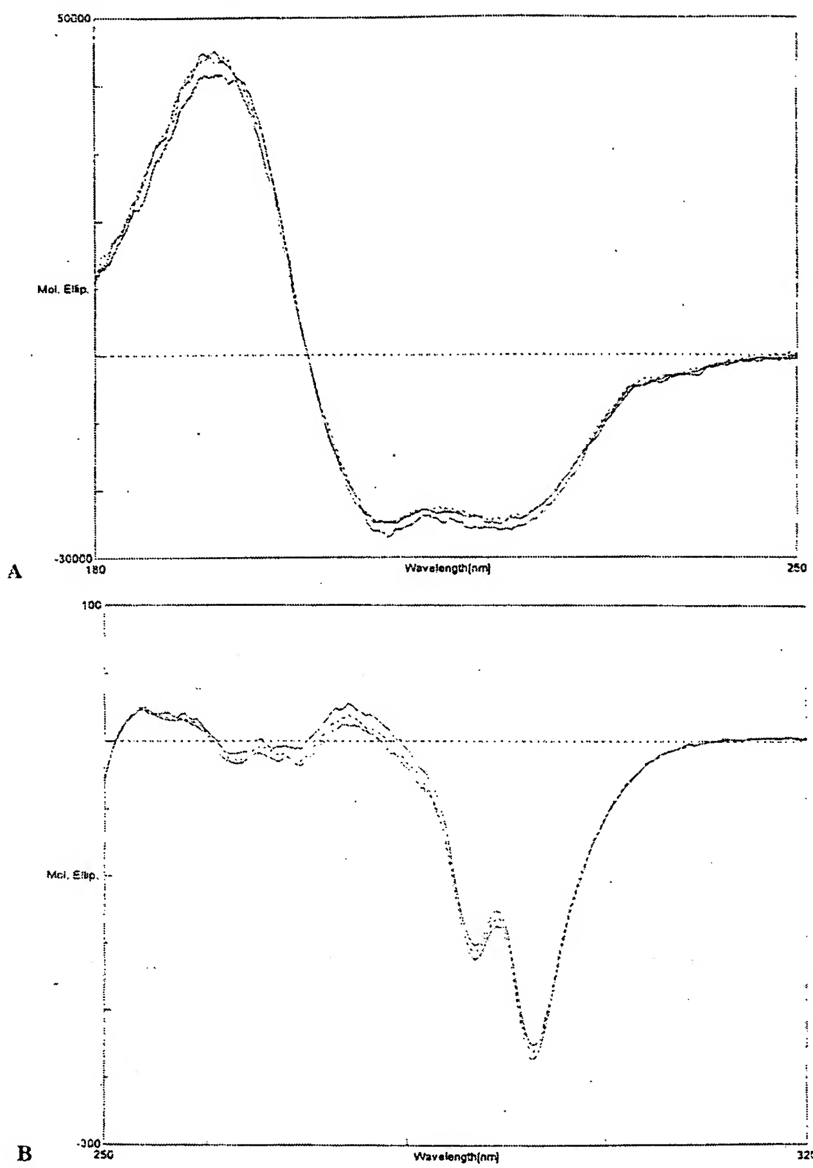


FIG. 3. Circular dichroism spectra of consensus interferon subforms. Consensus interferon was fractionated using an anion exchange column, as shown in Figure 2. Samples were dialyzed into 10 mM sodium phosphate, pH 7.4. Measurements were made on a Jasco J-170 spectopolarimeter, in a cell thermostat at 15°C. (——), acylated form; (– –), cys terminal form; (- - - -), met terminal form. A. Far UV spectrum. B. Near UV spectrum.

Fig 6-B Circular Dichroism spectrum of Infergen From Reference[Journal of Interferon and cytokine Research. 16:489-499(1996)]

Figure 6-C

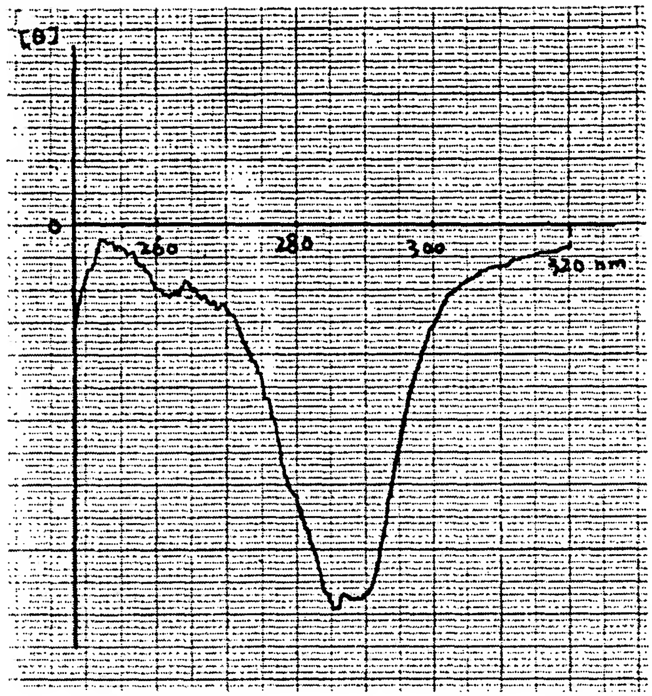


Fig 6-C Circular Dichroism spectrum of rSIFN-co

Spectrum range: 320nm-250nm

Sensitivity: 2 m°/cm

Light path: 2cm

Equipment: Circular Dichroism J-500C

Samples : contain 0.5mg/ml rSIFN-co, 5.9 mg/ml of NaCl and 3.8 mg/ml of Na_2PO_4, pH7.0.

Figure 6-D

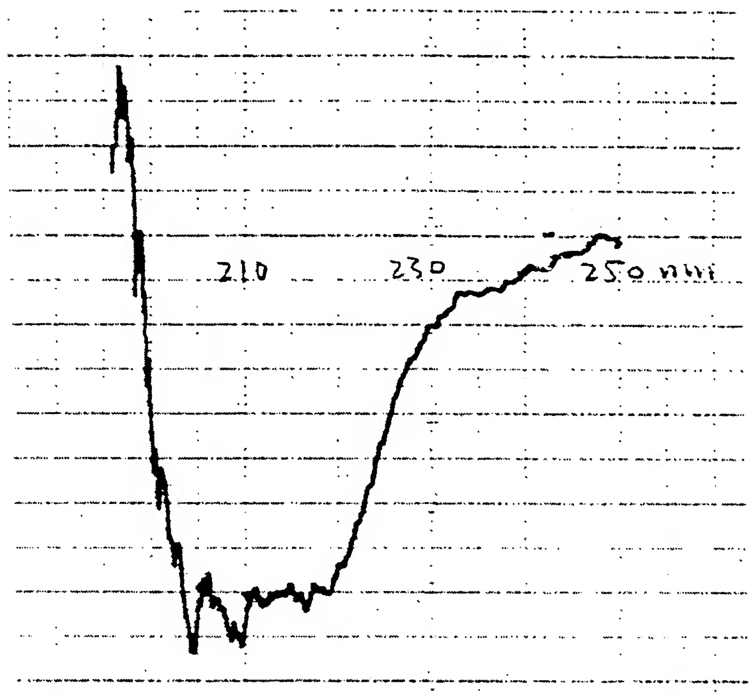


Fig 6-D Circular Dichroism spectrum of rSIFN-co

Spectrum range: 250nm – 190nm

Sensitivity: 2 m°/cm

Light path: 0.20 cm

Equipment: Circular Dichroism J-500C

Samples :contain 30μg/ml rSIFN-co, 5.9 mg/ml of NaCl and 3.8 mg/ml of Na_2PO_4, pH7.0.